

SEQUENCE LISTING

SEQ ID NO: 1:

GGCTCCTCATCTGGAACACCTCGGGTCACCCCCGACAACGGTGGTGGGAGGGAGAGCGGC	60
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GTGCACACCTACCAGACGGAGAAGCAGAGGAGGAAGCAGCACCTCAGCCCGCGGAGGTG	300
GAGGCCATCCTGCAGGTCATCCAGAGGGCAGAGCGGCTCGACGTCTGGAGCAGCAGAGA	360
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CGGTGGGGCTATCTCCGTTGCTATATTAATGGCAAGACTAAATGAAACCTAGGGCACGGC	1440
CTCCGAAGCTGCGTGTGGCCCCCTTAGAGGTGAGCATCAGAGCCAGAGCAGTGAGGGGGAG	1500
ACTCACCCACCCTCTCCCTCTCCCTTCAGCTCTGGGAGGCAGGCGCAGTGCCCCCTCCC	1560
ATGGGCTGGCCCAGGACCGCGGTGAAACCTGGGTCTGTTTAGTTTCTTTGGTTTTTGTA	1620
TGTTTGTGTTGTTTTTGACACAGTCTCGCTTGTGTCAGGCTGGGGTGCAGTGGCACGA	1680
TCGCGGCTCACTGCAACCTCCACCTCCCGGGCTCAAGCGATTCTCTCACCTCAGCCTCCT	1740
GAGTAGGTGGGATTACAGATGCCCCGCCACCACCCAGTTAATTTTTGTATTTTTAGAAG	1800
AGATGGGGTTTCTCCATGTTGGCCAGGCTGGTCTTGAACCTCTGGTCTCAAGTGATCCGC	1860
CCGCCTCGGCCTCCCAAAGTGTGGGATTACAGGTGTGAGCCACCGCACCAATCCTATT	1920
AGGTTTCTTTGAATCCCCTCATGGCCTGCCTGGTTTTTGCTCAGCCTGTCTTCAGCTTGA	1980

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GGAGCTGGGAAGCTCTGGTGGATGCTATGAACTCACTTGCTGAAGAGCAGCGTTCAGGTG	2040
CATCCCCAGCCAGGGCACGTGGCTCCCTCAGCCATGAATTCATTCTCTTCAGGAGGTTT	2100
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TGAAGAGAGAGAACGTGTGTGTGTGTGTGCGGTGATCACACCCTCCCATCCTTCCTGCCTC	2220
CTGCCCCAAACCCCGGGTTCCTGGGTCTGGAAGGGCCTTCTCTCCAAGCTGGGAGCTCCT	2280
GGGCCCCCACCATTCACTTTTTGTCTCTGCTGCTGGCAAACAGTAAAGAACTCACTTTC	2340
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SEQ ID NO: 2:

MetAlaAspThrIlePheGlySerGlyAsnAspGlnTrpValCysProAsnAspArgGln	20
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GlnArgArgLysGlnHisLeuSerProAlaGluValGluAlaIleLeuGlnValIleGln	60
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GluThrMetArgArgAsnValMetGlyAsnGlyLeuSerGlnCysLeuLeuCysGlyGlu	100
ValLeuGlyPheLeuGlySerSerSerValPheCysLysAspCysArgLysValTrpLys	120
ArgSerGlyAlaTrpPheTyrLysGlyLeuProLysTyrIleLeuProLeuLysThrPro	140
GlyArgAlaAspGluProGlnPheArgProTrpProThrGluProAlaGluArgGluPro	160
ArgSerSerGluThrSerArgIleTyrThrTrpAlaArgGlyArgValValSerSerAsp	180
SerAspSerAspSerAspLeuSerSerSerSerLeuGluAspArgLeuProSerThrGly	200
ValArgAspArgLysGlyAspLysProTrpLysGluSerGlyGlySerValGluAlaPro	220
ArgMetGlyPheThrGlnProAlaGlyHisLeuPheGlyLeuGlnSerSerLeuAlaSer	240
GlyGluThrGlyThrGlySerAlaAspProProGlyGlyGlyThrGlySerAlaAspPro	260
ProGlyGlyProArgProGlyLeuThrArgArgAlaProValLysAspThrProGlyArg	280
AlaProAlaAlaAspAlaAlaProAlaGlyProSerSerCysLeuGly	296

SEQ ID NO: 3:

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TGGGTTTGCCCCAATGACCGGCAGCTTGCCCTTCGAGCCAAGCTGCAGACGGGCTGGTCC	240
GTGCACACCTACCAGACGGAGAAGCAGAGGAGGAAGCAGCACCTCAGCCCCGGCGGAGGTG	300
GAGGCCATCCTGCAGGTCATCCAGAGGGCAGAGCGGCTCGACGTCCTGGAGCAGCAGAGA	360
ATCGGGCGGCTGGTGGAGCGGCTGGAGACCATGAGGCGGAATGTGATGGGGAACGGCCTG	420
TCCCAGTGTCTGCTCTGCGGGGAGGTGCTGGGCTTCCTGGGCAGCTCGTCCGTGTTCTGC	480

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CGGCCCCCTGTGGCTGTGTAAGATCTGCAGTGAGCAAAGAGAGGTCTGGAAGAGGTGCGGG	600
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GATGACCCCCACTTCCGACCTTTGCCACGGAACCGGCAGAGCGAGAGCCCAGAAGCTCT	720
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CAGACTTCCCTGTGGAGGATTCTTGCCAGACCCTGCCCCGGCTCCTCCCTGACCGGTCTTT	1200
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CCTCCCCAGCTCAGTGCCTTTCTGCACCCCTTCTCTCCTGGGGAGCTGTCTGCATCCGCC	1320
ACCCCTCCAACCACTGCCCTCAGCCCCCGACCTTATTTATTACCCTCCCCCTCCACACC	1380
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CATCAGAGCCAGAGCAGTGAGGGGGAGACTCACCCACCCTCTCCCTCTCCCTTCAGCTCT	1620
GGGAGGCAGGCGCAGTGCCCCCTCCCATGGGCTGGCCCAGGACCGCGGGTGAAACCTGG	1680
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TGCCCAGGCTGGGGTGCAGTGGCACGATCGCGGCTCACTGCAACCTCCACCTCCCGGGCT	1800
CAAGCGATTCTCTCACCTCAGCCTCCTGAGTAGGTGGGATTACAGATGCCCCGCCACCACA	1860
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CACTTGCTGAAGAGCAGCGTTCAGGTGCATCCCCAGCCAGGGCACGTGGCTCCCTCAGCC	2160
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SEQ ID NO: 4:

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GlnArgArgLysGlnHisLeuSerProAlaGluValGluAlaIleLeuGlnValIleGln 60
ArgAlaGluArgLeuAspValLeuGluGlnGlnArgIleGlyArgLeuValGluArgLeu 80
GluThrMetArgArgAsnValMetGlyAsnGlyLeuSerGlnCysLeuLeuCysGlyGlu 100
ValLeuGlyPheLeuGlySerSerSerValPheCysLysAspCysArgLysLysValCys 120
ThrLysCysGlyIleGluAlaSerProGlyGlnLysArgProLeuTrpLeuCysLysIle 140
CysSerGluGlnArgGluValTrpLysArgSerGlyAlaTrpPheTyrLysGlyLeuPro 160
LysTyrIleLeuProLeuLysThrProGlyArgAlaAspAspProHisPheArgProLeu 180
ProThrGluProAlaGluArgGluProArgSerSerGluThrSerArgIleTyrThrTrp 200
AlaArgGlyArgValValSerSerAspSerAspSerAspSerAspLeuSerSerSerSer 220
LeuGluAspArgLeuProSerThrGlyValArgAspArgLysGlyAspLysProTrpLys 240
GluSerGlyGlySerValGluAlaProArgMetGlyPheThrGlnProAlaGlyHisLeu 260
PheGlyLeuGlnSerSerLeuAlaSerGlyGluThrGlyThrGlySerAlaAspProPro 280
GlyGlyGlyThrGlySerAlaAspProProGlyGlyProArgProGlyLeuThrArgArg 300
AlaProValLysAspThrProGlyArgAlaProAlaAlaAspAlaAlaProAlaGlyPro 320
SerSerCysLeuGly 325

SEQ ID NO: 5:

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TGGTCCGTGCACACCTACCAGACGGAGAAGCAGAGGAGGAAGCAGCACCTCAGCCCGGCG 360
GAGGTGGAGGCCATCCTGCAGGTCATCCAGAGGGCAGAGCGGCTCGACGTCCTGGAGCAG 420
CAGAGAATCGGGCGGCTGGTGGAGCGGCTGGAGACCATGAGGCGGAATGTGATGGGGAAC 480
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CAGAAGCGGCCCCCTGTGGCTGTGTAAGATCTGCAGTGAGCAAAGAGAGGTCTGGAAGAGG 660
TCGGGGGCGCTGGTTCTACAAAGGGCTCCCCAAGTATATCTTGCCCCCTGAAGACCCCTGGC 720
CGAGCTGATGACCCCCACTTCCGACCTTTGCCCACGGAACCGGCAGAGCGAGAGCCCAGA 780
AGCTCTGAGACCAGCCGCATCTACACGTGGGCCCCGAGGAAGAGTGGTTTCCAGTGACAGT 840
GACAGTGA CTGGATCTTAGCTCCTCCAGCCTAGAGGACAGACTCCCATCCACTGGGGTC 900

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AGGGACCGGAAAGGCGACAAACCCTGGAAGGAGTCAGGTGGCAGCGTGGAGGCCCCCAGG 960
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 CGTCTGCCTCCCCAGCTCAGTGCCTTTCTGCACCCCTTCTCTCCTGGGGAGCTGTCTGCA 1380
 TCCGCCACCCCTCCAACCACTGCCCTCAGCCCCCGACCTTATTTATTACCCTCCCCTCC 1440
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 AGCTCTGGGAGGCAGGCGCAGTGCCCCCTCCCATGGGCTGGCCAGGACCGCGGGTGAA 1740
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 CTTTGTGCCCAGGCTGGGGTGCAGTGGCACGATCGCGGCTCACTGCAACCTCCACCTCC 1860
 CGGGCTCAAGCGATTCTCTCACCTCAGCCTCCTGAGTAGGTGGGATTACAGATGCCCGCC 1920
 ACCACACCCAGTTAATTTTTGTATTTTTAGAAGAGATGGGGTTTCTCCATGTTGGCCAGG 1980
 CTGGTCTTGAACCTCCTGGTCTCAAGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGA 2040
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 TGAACCTACTTGCTGAAGAGCAGCGTTCAGGTGCATCCCCAGCCAGGGCACGTGGCTCCC 2220
 TCAGCCATGAATTCACTTCTCTTCAGGAGGTTTGGCTTGGCATGAAAATACTTCATTAG 2280
 AGTATGGGCAAATGCTTCTGGAAAACCCCTTCCCTGAAGAGAGAGAACGTGTGTGTGTG 2340
 TCGGTGATCACACCCTCCCATCCTTCCCTGCCTCCTGCCCCAAACCCCGGGTTCCTGGGTC 2400
 TGGAAGGGCCTTCTCTCCAAGCTGGGAGCTCCTGGGCCCCCACCATTCACTTTTTGTCTT 2460
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 AAACAATGAAGATTAAAA 2538

SEQ ID NO: 6:

MetArgArgAsnValMetGlyAsnGlyLeuSerGlnCysLeuLeuCysGlyGluValLeu 20
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 CysGlyIleGluAlaSerProGlyGlnLysArgProLeuTrpLeuCysLysIleCysSer 60
 GluGlnArgGluValTrpLysArgSerGlyAlaTrpPheTyrLysGlyLeuProLysTyr 80
 IleLeuProLeuLysThrProGlyArgAlaAspAspProHisPheArgProLeuProThr 100
 GluProAlaGluArgGluProArgSerSerGluThrSerArgIleTyrThrTrpAlaArg 120

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GlyArgValValSerSerAspSerAspSerAspSerAspLeuSerSerSerSerLeuGlu	140
AspArgLeuProSerThrGlyValArgAspArgLysGlyAspLysProTrpLysGluSer	160
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CysLeuGly	243

SEQ ID NO: 7:

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TCCCAGTGTCTGCTCTGCGGGGAGGTGCTGGGCTTCCTGGGCAGCTCGTCGGTGTCTGC	480
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CCCACATGCAGTGTGAGAGGGGCGCCCGGTGGGGCTATCTCCGTTGCTATATTAATGGC	1620

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CATCAGAGCCAGAGCAGTGAGGGGGAGACTACCCACCCTCTCCCTCTCCCTTCAGCTCT	1740
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TGCCCAGGCTGGGGTGCACTGGCACGATCGCGGCTCACTGCAACCTCCACCTCCCCGGGCT	1920
CAAGCGATTCTCTCACCTCAGCCTCCTGAGTAGGTGGGATTACAGATGCCCCGCCACCACA	1980
CCCAGTTAATTTTTGTATTTTAGAAGAGATGGGGTTTCTCCATGTTGGCCAGGCTGGTC	2040
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GTGTGAGCCACCGCACCCAATCCTATTAGGTTTCTTTGAATCCCCTCATGGCCTGCCTGG	2160
TTTTTGCTCAGCCTGTCTTCAGCTTGAGGAGCTGGGAAGCTCTGGTGGATGCTATGAACT	2220
CAGTTGCTGAAGAGCAGCGTTCAGGTGCATCCCCAGCCAGGGCACGTGGCTCCCTCAGCC	2280
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GGCAATGCTTCTGGAAAACCTTCCCTGAAGAGAGAGAACGTGTGTGTGTGTGCGGTG	2400
ATCACACCTCCCATCCTTCTGCCTCCTGCCCCAAACCCCGGGTTCCTGGGTCTGGAAG	2460
GGCCTTCTCTCAAGCTGGGAGCTCCTGGGCCCCCACCATTCACTTTTTGTCTTGCTGC	2520
TGGCAAACAGTAAAGAACTCACTTTCCCTGTGGCACGTTATGCTTCAGAATTAAACAA	2580
TGAAGATTAAAA	2592

SEQ ID NO: 8:

MetAlaAspThrIlePheGlySerGlyAsnAspGlnTrpValCysProAsnAspArgGln	20
LeuAlaLeuArgAlaLysLeuGlnThrGlyTrpSerValHisThrTyrGlnThrGluLys	40
GlnArgArgLysGlnHisLeuSerProAlaGluValGluAlaIleLeuGlnValIleGln	60
ArgAlaGluArgLeuAspValLeuGluGlnGlnArgIleGlyArgLeuValGluArgLeu	80
GluThrMetArgArgAsnValMetGlyAsnGlyLeuSerGlnCysLeuLeuCysGlyGlu	100
ValLeuGlyPheLeuGlySerSerSerValPheCysLysAspCysArgLysLysValCys	120
ThrLysCysGlyIleGluAlaSerProGlyGlnLysArgProLeuTrpLeuCysLysIle	140
CysSerGluGlnArgGluValTrpLysArgSerGlyAlaTrpPheTyrLysGlyLeuPro	160
LysTyrIleLeuProLeuLysThrProGlyArgAlaAspAspProHisPheArgProLeu	180
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AlaArgGlyArgValValGlyArgLysCys	210

SEQ ID NO: 9:

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CTTTGTTGCCAGGCTGGGGTGACGTGGCACGATCGCGGCTCACTGCAACCTCCACCTCC	1980
CGGGCTCAAGCGATTCTCTCACCTCAGCCTCCTGAGTAGGTGGGATTACAGATGCCCCGCC	2040
ACCACACCCAGTTAATTTTTGTATTTTTAGAAAGAGATGGGGTTTCTCCATGTTGGCCAGG	2100
CTGGTCTTGAACCTCTGGTCTCAAGTGATCCGCCCCGCTCGGCCTCCCAAAGTGCTGGGA	2160
TTACAGGTGTGAGCCACCGACCCAATCCTATTAGGTTTCTTTGAATCCCCTCATGGCCT	2220
GCCTGGTTTTTTGCTCAGCCTGTCTTCAGCTTGAGGAGCTGGGAAGCTCTGGTGGATGCTA	2280
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TCAGCCATGAATTCACTTCTCTTCAGGAGGTTTGGCTTGGCATGAAAATACTTCATTCAG 2400
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TCGGTGATCACACCCCTCCCATCCTTCCCTGCCTCCTGCCCCAAACCCCGGGTTCCTGGGTC 2520
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TGCTGCTGGCAAACAGTAAAGAACTCACTTTCCCTGTGGCACGTTATGCTTCAGAATTA 2640
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SEQ ID NO: 10:

MetArgArgAsnValMetGlyAsnGlyLeuSerGlnCysLeuLeuCysGlyGluValLeu 20
GlyPheLeuGlySerSerSerValPheCysLysAspCysArgLysLysValCysThrLys 40
CysGlyIleGluAlaSerProGlyGlnLysArgProLeuTrpLeuCysLysIleCysSer 60
GluGlnArgGluValTrpLysArgSerGlyAlaTrpPheTyrLysGlyLeuProLysTyr 80
IleLeuProLeuLysThrProGlyArgAlaAspAspProHisPheArgProLeuProThr 100
GluProAlaGluArgGluProArgSerSerGluThrSerArgIleTyrThrTrpAlaArg 120
GlyArgValValGlyArgLysCys 128